



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy
Search <u>Protein</u> <input type="button" value="v"/> for _____						
		Limits	Preview/Index	History	Clipboard	
Display	<u>GenPept</u> <input type="button" value="v"/>	Save	Text	Add to Clipboard		

☐ 1: P02932. OUTER MEMBRANE
PO...[gi:130121]

BLink, Related Sequences, PubMed,
Taxonomy, LinkOut

LOCUS PHOE_ECOLI 351 aa BCT
 DEFINITION OUTER MEMBRANE PORE PROTEIN E PRECURSOR.
 ACCESSION P02932
 PID g130121
 VERSION P02932 GI:130121
 DBSOURCE swissprot: locus PHOE_ECOLI, accession P02932;
 class: standard.
 created: Jul 21, 1986.
 sequence updated: Jul 21, 1986.
 annotation updated: Aug 20, 2001.
 xrefs: gi: gi: 42389, gi: gi: 42391, gi: gi: 236
1786436, gi: gi: 4902908, gi: gi: 4902976, gi: g
1552809, gi: gi: 42495, gi: gi: 42496, gi: gi: 7
443180
 xrefs (non-sequence databases): SWISS-2DPAGE P02
 B037.0, EcoGene EG10729, InterPro IPR001702, Pfa
 PR00182, PRINTS PR00183, PROSITE PS00576
 KEYWORDS Outer membrane; Transmembrane; Porin; Signal; 3D
 Complete proteome.
 SOURCE Escherichia coli.
 ORGANISM Escherichia coli
 Bacteria; Proteobacteria; gamma subdivision; Ent
 Escherichia.
 REFERENCE 1 (residues 1 to 351)
 AUTHORS Overbeeke,N., Bergmans,H., van Mansfeld,F. and L
 TITLE Complete nucleotide sequence of phoE, the struct
 phosphate limitation inducible outer membrane po
 Escherichia coli K12
 JOURNAL J. Mol. Biol. 163 (4), 513-532 (1983)
 MEDLINE 83189086
 REMARK SEQUENCE FROM N.A.
 STRAIN=K12
 REFERENCE 2 (residues 1 to 351)
 AUTHORS Blattner,F.R., Plunkett,G.I.I.I., Bloch,C.A., Pe

Burland,V., Riley,M., Collado-Vides,J., Glasner,
Mayhew,G.F., Gregor,J., Davis,N.W., Kirkpatrick,
Rose,D.J., Mau,B. and Shao,Y.

TITLE The complete genome sequence of Escherichia coli
JOURNAL Science 277 (5331), 1453-1474 (1997)
MEDLINE 97426617
REMARK SEQUENCE FROM N.A.
STRAIN=K12 / MG1655

REFERENCE 3 (residues 1 to 351)
AUTHORS Takemoto,K., Mori,H., Murayama,N., Kataoka,K., Y
Yamamoto,Y., Inokuchi,H., Miki,T., Hatada,E., Fu
Ichihara,S., Mizuno,T., Makino,K., Nakata,A., Yu
and Mizobuchi,K.

TITLE Direct Submission
JOURNAL Submitted (??-FEB-1996)
REMARK SEQUENCE FROM N.A.
STRAIN=K12 / W3110

REFERENCE 4 (residues 1 to 351)
AUTHORS Schramm,S., Duncan,M., Allen,E., Araujo,R., Apar
Davis,K., Federspiel,N., Hyman,R., Kalman,S., Ko
Lashkari,D., Lew,H., Lin,D., Namath,A., Oefner,P
Davis,R.W.

TITLE Direct Submission
JOURNAL Submitted (??-SEP-1996)
REMARK SEQUENCE FROM N.A.

REFERENCE 5 (residues 1 to 351)
AUTHORS Deutch,A.H., Rushlow,K.E. and Smith,C.J.

TITLE Analysis of the Escherichia coli proBA locus by
sequencing
JOURNAL Nucleic Acids Res. 12 (15), 6337-6355 (1984)
MEDLINE 84297232
REMARK SEQUENCE OF 1-22 FROM N.A.

REFERENCE 6 (residues 1 to 351)
AUTHORS Struyve,M., Moons,M. and Tommassen,J.

TITLE Carboxy-terminal phenylalanine is essential for
assembly of a bacterial outer membrane protein
JOURNAL J. Mol. Biol. 218 (1), 141-148 (1991)
MEDLINE 91162638
REMARK MUTAGENESIS OF PHE-351.

REFERENCE 7 (residues 1 to 351)
AUTHORS Jap,B.K., Walian,P.J. and Gehring,K.

TITLE Structural architecture of an outer membrane cha
by electron crystallography
JOURNAL Nature 350 (6314), 167-170 (1991)
MEDLINE 91172301
REMARK X-RAY CRYSTALLOGRAPHY (6.0 ANGSTROMS).

REFERENCE 8 (residues 1 to 351)
AUTHORS Cowan,S.W., Schirmer,T., Rummel,G., Steiert,M.,
Pauptit,R.A., Jansonius,J.N. and Rosenbusch,J.P.
TITLE Crystal structures explain functional properties
porins
JOURNAL Nature 358 (6389), 727-733 (1992)
MEDLINE 92375189
REMARK X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
REFERENCE 9 (residues 1 to 351)
AUTHORS Struyve,M., Visser,J., Adriaanse,H., Benz,R. and
TITLE Topology of PhoE porin: the 'eyelet' region
JOURNAL Mol. Microbiol. 7 (1), 131-140 (1993)
MEDLINE 93172954
REMARK TOPOLOGY.

COMMENT

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in collaboration between the Swiss Institute of Bioinformatics
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The original entry is available from <http://www.ebi.ac.uk/sprot>

[FUNCTION] THIS IS ONE OF THE PROTEINS INDUCED WHEN
BACTERIA ARE GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN
IS PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC
PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVE
SOLUTES.

[SUBUNIT] HOMOTRIMER.

[SUBCELLULAR LOCATION] INTEGRAL MEMBRANE PROTEIN

[SIMILARITY] BELONGS TO THE OMPC/PHOE FAMILY OF

FEATURES

	Location/Qualifiers
source	1..351 /organism="Escherichia coli" /db_xref="taxon:562"
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Region	22..351 /region_name="Mature chain" /note="OUTER MEMBRANE PORE PROTEIN E."
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Region	/region_name="Hydrogen bonded turn" 93..104
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Region	/region_name="Helical region" 124..126
Region	/region_name="Hydrogen bonded turn" 140..141
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Site        /region_name="Beta-strand region"
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            /note="F->Y,N,S,V: LESS RESISTANT TO TR
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ORIGIN

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181 vkkqngdgfg tsltydfggs dfaisgaytn sdrtnegnlq srgtgk
241 niylatfyse trkmtpitgg fanktqnfea vaqqqfdfgl rpslgy
301 dlvnyidvga tyyfnknmsa fvdykinql d sdnklninnd divavg
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Revised: October 24, 2001.

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